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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Atty. Docket No: 16313-0037

In re patent application of

COSTA E SILVA, OSWALDO DA et al.

Serial No. 09/828,447

Filed: April 6, 2001

For: SIGNAL TRANSDUCTION STRESS-RELATED PROTEINS AND METHODS
OF USE IN PLANTS

STATEMENT TO SUPPORT FILING AND SUBMISSION IN
ACCORDANCE WITH 37 C.F.R. §§ 1.821-1.825

Assistant Commissioner for Patents
Washington, D.C. 20231
Box SEQUENCE

Sir:

In connection with a Sequence Listing submitted concurrently
herewith, the undersigned hereby states that:

1. the submission, filed herewith in accordance with 37
C.F.R. § 1.821(g), does not include new matter;

2. the content of the attached paper copy and the
attached computer readable copy of the Sequence Listing, submitted in
accordance with 37 C.F.R. § 1.821(c) and (e), respectively, are the same;
and


3. all statements made herein of their own knowledge are
true and that all statements made on information and belief are believed to
be true; and further, that these statements were made with the knowledge
that willful false statements and the like so made are punishable by fine
or imprisonment, or both, under Section 1001 of Title 18 of the United

09/828,447

[illegible]

Date 25, 2001

Respectfully submitted,



James A. Coburn



#6

1/21

SEQUENCE LISTING

<110> COSTA E SILVA, OSWALDO DA
BOHNERT, HANS J.
VAN THIELEN, NOCHA
CHEN, ROUYING
ISHITANI, MANABU

<120> SIGNAL TRANSDUCTION STRESS-RELATED PROTEINS AND METHODS
OF USE IN PLANTS

<130> 16313-0037

<140> 09/828,447

<141> 2001-04-06

<150> 60/196,001

<151> 2000-04-07

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Glu Lys Cys Ile Lys Ala Ile Lys Ala Asn Ala Phe Val Ser Ser Lys
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Pro	Val	Ala	Phe	Glu	Lys	Cys	Ile	Lys	Ala	Ile	Lys	Ala	Asn	Ala	Phe
595						600						605			
Val	Ser	Ser	Lys	Tyr	Pro	Val	Val	Ile	Thr	Leu	Glu	Asp	His	Leu	Ser
610						615						620			
Ser	Pro	Leu	Gln	Ala	Leu	Ala	Ala	Glu	Thr	Leu	Thr	Asn	Ile	Leu	Gly
625						630						635			
Glu	Asp	Leu	Tyr	Tyr	Pro	Pro	Ser	Ser	Asp	Gly	Phe	Lys	Glu	Leu	Pro
			645						650			655			
Ser	Pro	Glu	Ser	Leu	Lys	Gly	Lys	Ile	Leu	Ile	Ser	Thr	Lys	Pro	Pro
			660						665			670			
Lys	Glu	Tyr	Leu	Glu	Ala	Ala	Val	Ala	Gln	Lys	Ser	Ala	Leu	Lys	Asp
675						680						685			
Glu	Lys	Ile	Leu	Asn	Glu	Phe	Lys	Lys	Ala	Asp	Lys	Leu	Gln	Glu	Gln
690						695						700			
Ser	Thr	Ala	Pro	Val	Lys	Ser	Pro	Val	Glu	Lys	Lys	Ile	Ala	Val	Pro
705						710						715			
Pro	Ser	Glu	Lys	Thr	Lys	Ser	Ile	Ser	Glu	Glu	Lys	Asp	Leu	Ser	Glu
			725						730			735			
Lys	Val	Gly	Asn	Leu	Arg	Val	Asp	Ser	Glu	Gly	Glu	Ser	Ala	Asp	Pro
			740						745			750			
Ala	Pro	Ala	Ser	Ser	Pro	Asp	Gly	Lys	Lys	Ala	Thr	Leu	Thr	Ala	Asp
755						760						765			
Ser	Glu	Ser	Asp	Asp	Asp	Asp	Asn	Lys	Lys	Asn	Pro	Glu	Tyr	Ala	Arg
770						775						780			
Leu	Ile	Thr	Ile	His	Gln	Ser	Lys	Pro	Ser	Lys	Gly	Thr	Thr	Val	Glu
785						790						795			
Asp	Arg	Leu	Lys	Val	Glu	Gly	Thr	Val	Val	Arg	Ile	Ser	Leu	Ser	Glu
			805						810			815			
Thr	Lys	Leu	Glu	Lys	Val	Thr	Glu	Glu	Phe	Pro	Glu	Leu	Val	Val	Lys
			820						825			830			

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Phe Thr Gln Arg Asn Ile Leu Arg Val Tyr Pro Ala Gly Asn Arg Val
835 840 845

Asn Ser Ser Asn Tyr Asp Pro Thr Ala Ala Trp Ile His Gly Ala Gln
850 855 860

Met Val Ala Gln Asn Met Gln Gly Tyr Gly Lys Glu Leu Trp Gln Ala
865 870 875 880

His Gly Lys Phe Arg Gly Asn Gly Gly Cys Gly Tyr Ile Leu Lys Pro
885 890 895

Lys Tyr Leu Leu Glu Asp Leu Pro Asn Gly Lys Pro Phe Asn Pro Ser
900 905 910

Ala Pro Gly Asp Thr Lys Met Ile Leu Lys Val Lys Val Met Thr Thr
915 920 925

Met Gly Trp Asp Lys Ala Phe Pro Lys Tyr His Phe Asp Leu Phe Ser
930 935 940

Pro Pro Asp Phe Phe Thr Arg Leu Leu Val Thr Gly Val Pro Ala Asp
945 950 955 960

Val Ala Lys Trp Lys Thr Ser Val Ile Asp Asp Val Trp Glu Pro His
965 970 975

Trp Asn Glu Asp His Glu Phe Tyr Leu Lys Cys Pro Glu Leu Ala Leu
980 985 990

Leu Arg Ile Glu Val Arg Asp His Asp Glu Glu Ser Gln Asp Glu Phe
995 1000 1005

Glu Gly Gln Ala Cys Leu Pro Met His Glu Ile Lys Asp Gly Tyr Arg
1010 1015 1020

Cys Val Gln Met Tyr Asp Lys Lys Gly Ser Val Leu Lys Gly Val Lys
1025 1030 1035 1040

Met Leu Phe His Phe Gln Lys Arg Ser Phe Ser Pro Val Gln
1045 1050

<210> 12

<211> 628

<212> PRT

<213> Physcomitrella patens

<400> 12

Met Cys Ser Ile Ala Cys Cys Arg Ser Gly Thr Pro Lys Gly Asp Pro
1 5 10 15

Glu Gln Asp Leu Val Gly Glu Val Phe Thr Ile Tyr Ser Glu Asn Glu
20 25 30

Arg Met Ser Ala Glu Gly Leu Leu Lys Phe Leu His Thr Glu Gln Gly
35 40 45

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
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Asp	Val	Asp	Phe	Thr	Leu	Asp	Asp	Ala	Lys	Gln	Ile	Met	Glu	Arg	Ile
50						55					60				
Arg	Lys	Asp	Trp	Lys	Lys	Ser	Phe	Gly	Leu	Ala	Ser	Ile	Asn	Ser	Asp
65					70					75					80
Leu	Ser	Lys	Glu	Ala	Phe	Arg	Lys	Tyr	Leu	Met	Asn	Pro	Asp	Leu	Asn
				85					90					95	
Gly	Val	Leu	His	Asn	Val	Val	His	Gln	Asp	Met	Thr	Gln	Pro	Met	Ser
			100					105					110		
His	Tyr	Phe	Ile	Phe	Thr	Gly	His	Asn	Ser	Tyr	Leu	Thr	Gly	Asn	Gln
		115					120					125			
Leu	Ser	Ser	Asp	Ser	Ser	Asp	Thr	Pro	Ile	Ala	Ala	Ala	Leu	Arg	Arg
		130				135					140				
Gly	Val	Arg	Val	Val	Glu	Leu	Asp	Leu	Trp	Pro	Asp	Asp	Lys	Gly	Gly
145					150					155					160
Met	Lys	Val	Thr	His	Gly	Asn	Thr	Leu	Thr	Asn	Pro	Val	Ser	Phe	Gln
				165					170					175	
Lys	Cys	Val	Thr	Ala	Ile	Lys	Asn	Asn	Ala	Phe	Phe	Thr	Ser	Glu	Tyr
			180				185						190		
Pro	Val	Cys	Val	Thr	Ile	Glu	Asp	His	Leu	Thr	Ser	Glu	Leu	Gln	Gly
		195					200					205			
His	Ala	Ala	Glu	Ile	Leu	Glu	Gln	Ile	Leu	Gly	Asp	Ala	Leu	Tyr	Tyr
	210					215					220				
Pro	Pro	Thr	Thr	Asp	Ala	Leu	Val	Glu	Phe	Pro	Ser	Pro	Glu	Ser	Leu
225					230					235					240
Lys	Arg	Lys	Ile	Ile	Ile	Ser	Thr	Lys	Pro	Pro	Lys	Glu	Tyr	Leu	Glu
				245					250					255	
Ala	Cys	Ser	Thr	Gln	Lys	Leu	Ala	Met	Glu	Asn	Arg	Asn	Leu	Val	Glu
			260					265					270		
Glu	Leu	Glu	Lys	Glu	Asp	Lys	Leu	Glu	Gln	Thr	Thr	Phe	Ala	Pro	Leu
			275				280					285			
Glu	Glu	Asn	His	Ile	Leu	Gly	Glu	Asn	Thr	Pro	Ser	Leu	Arg	Lys	Glu
		290				295					300				
Val	Glu	Val	Leu	Ser	Gln	Lys	Glu	Met	Ser	Thr	Pro	Ala	Glu	Leu	Asn
305					310						315				320
Ser	Arg	Ser	Pro	Ser	Asp	Leu	Gly	Glu	Ala	Thr	Ser	Thr	Arg	Tyr	Ser
				325					330					335	
Lys	Ser	Asn	Asp	Gly	Asn	Asp	Asn	Pro	Lys	His	Phe	Lys	Tyr	Ala	Arg
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<212> PRT
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<213> Physcomitrella patens

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Met Ser Thr Glu Lys Glu Arg Glu Ser Tyr Val Tyr Met Ala Lys Leu
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Ala Glu Gln Ala Glu Arg Tyr Asp Glu Met Val Glu Ser Met Lys Lys
 20 25 30

Val Ala Lys Leu Asp Val Glu Leu Thr Val Glu Glu Arg Asn Leu Leu
 35 40 45

Ser Val Gly Tyr Lys Asn Val Ile Gly Ala Arg Arg Ala Ser Trp Arg
 50 55 60

Ile Met Ser Ser Ile Glu Gln Lys Glu Glu Ser Lys Gly Asn Glu Gln
 65 70 75 80

Asn Val Lys Arg Ile Lys Asp Tyr Arg His Lys Val Glu Glu Glu Leu
 85 90 95

Ser Lys Ile Cys Asn Asp Ile Leu Ser Ile Ile Asp Gly His Leu Ile
 100 105 110

Pro Ser Ser Ser Thr Gly Glu Ser Thr Val Phe Tyr Tyr Lys Met Lys
 115 120 125

Gly Asp Tyr Tyr Arg Tyr Leu Ala Glu Phe Lys Thr Gly Asn Glu Arg
 130 135 140

Lys Glu Ala Ala Asp Gln Ser Leu Lys Ala Tyr Gln Ala Ala Ser Ser
 145 150 155 160

Thr Ala Val Thr Asp Leu Ala Pro Thr His Pro Ile Arg Leu Gly Leu
 165 170 175

Ala Leu Asn Phe Ser Val Phe Tyr Tyr Glu Ile Leu Asn Ser Pro Glu
 180 185 190

Arg Ala Cys His Leu Ala Lys Gln Ala Phe Asp Glu Ala Ile Ala Glu
 195 200 205

Leu Asp Thr Leu Ser Glu Glu Ser Tyr Lys Asp Ser Thr Leu Ile Met
 210 215 220

Gln Leu Leu Arg Asp Asn Leu Thr Leu Trp Thr Ser Asp Leu Gln Asp
 225 230 235 240

Glu Gly Gly Asp Asp Gln Gly Lys Gly Asp Asp Met Arg Pro Glu Glu
 245 250 255

Ala Glu

<210> 14

<211> 257

<212> PRT

<213> Physcomitrella patens

Met Thr Glu Leu Arg Glu Glu Asn Val Tyr Met Ala Lys Leu Ala Glu
1 5 10 15

Lys Ala Val Glu Asn Glu Glu Leu Thr Val Glu Glu Arg Asn Leu Leu
35 40 45

Ser Val Ala Phe Lys Asn Val Ile Gly Ala Arg Arg Ala Ser Trp Arg
50 55 60

Ile Ile Ser Ser Ile Glu Gln Lys Glu Glu Ala Lys Gly Ser Glu Glu
65 70 75 80

His Val Ala Ala Ile Lys Glu Tyr Arg Ser Lys Val Glu Ala Glu Leu
85 90 95

Ser Thr Ile Cys Asp Thr Ile Leu Lys Leu Leu Asp Ser His Leu Ile
100 105 110

Pro Ser Ser Thr Ser Gly Glu Ser Lys Val Phe Tyr Leu Lys Met Lys
115 120 125

Gly Asp Tyr His Arg Tyr Leu Ala Glu Phe Lys Ala Gly Ala Glu Arg
130 135 140

Lys Glu Ala Ala Glu Ala Thr Leu His Ala Tyr Lys His Ala Gln Asp
145 150 155 160

Ile Ser Thr Thr Glu Leu Ala Ser Thr His Pro Ile Arg Leu Gly Leu
165 170 175

Ala Leu Asn Phe Ser Val Phe Tyr Tyr Glu Ile Leu Val Ser Pro Asp
180 185 190

Arg Ala Cys His Leu Ala Lys Gln Ala Phe Asp Glu Ala Ile Ser Glu
195 200 205

Leu Asp Thr Leu Gly Glu Glu Ser Tyr Lys Asp Ser Thr Leu Ile Met
210 215 220

Gln Leu Leu Arg Asp Asn Leu Thr Leu Trp Thr Ser Asp Met Gln Asp
225 230 235 240

Asp Ile Gly Glu Glu Gly Lys Asp Ser Lys Val Glu Asp Ala Asp Asp
245 250 255

<210> 15

<211> 337

<212> PRT

<213> Physcomitrella patens

Met Ser Thr Glu Gly Gly Leu His Val Leu Asp Gly Ser Gln Ile Arg
1 5 10 15

Glu Gly Ser Lys Gly Tyr Leu Thr Pro Ser Glu Met Arg Gln Ala Ala
35 40 45

Ile Phe Glu Asn Ala Ala Ser Lys Leu Pro Thr Glu Asp Ser Ala Glu
65 70 75 80

Ile Ala Asp Ala Leu Glu Asp Glu Pro Val Val Val Ser Val Leu Asp
100 105 110

Val Ala Glu Asp Leu Phe Glu Lys Leu Asp Thr Asp Glu Ser Gly Lys
130 135 140

Gln Gly Val Pro Pro Ala Ala Ala Thr Thr Glu Ala Glu Glu Leu Val
165 170 175

Ala Gln Phe Ala Ala Leu Leu Gln Asp Val Leu Gln Asp Met Ala Glu
195 200 205

Asn Gly Ser His Leu Arg Lys Met Leu Ala Asp Glu Lys Ala Phe Lys
225 230 235 240

Arg Leu Ser Lys Ala Glu Ile Arg Pro Leu Phe Glu Gln Gln Thr Ala
260 265 270

Asp Glu Val Phe Lys Ala Val Asp Ser Asp Lys Ser Gly Glu Val Glu
290 295 300

Glu Thr Leu Arg Leu Asn Pro Ile Leu Val Glu Ile Glu Thr Ala Ser
325 330 335

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<210> 16
<211> 18
<212> DNA
<213> Artificial Sequence
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<400> 16
caggaaacag ctatgacc 18

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<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Primer

<400> 17
ctaaagggaa caaaagctg 19

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<210> 18
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<220>
<223> Description of Artificial Sequence: Primer

<400>	18	
tgtaaaacga cggccagt		18

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<210> 19
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<223> Description of Artificial Sequence: Primer

<400> 19
cagggtccgag ctgacgatga acccag 26

<210> 20
 <211> 33
 <212> DNA
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<220>
 <223> Description of Artificial Sequence: Primer

<400> 20
 atcccgggca atcgtcgggt gacattcctg ttc 33

<210> 21
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 21
 gcgttaacca acacctcagc gttccacatg cat 33

<210> 22
 <211> 26
 <212> DNA
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<220>
 <223> Description of Artificial Sequence: Primer

<400> 22
 cgagctcctc caccagattc ctgttc 26

<210> 23
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 23
 atcccgggct tcgggagttt aagaggatgt cacg 34

<210> 24
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 24
 gcgttaacct tgggtgcaca cactaaactg gtc 33

<220>
<223> Description of Artificial Sequence: Primer

<400> 29
gcgagctcca gcctcaactt agtcgcctgg aca 33

<210> 30
<211> 26
<212> DNA
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<223> Description of Artificial Sequence: Primer

<400> 30
ccctgctcaa cgcccagctg cataat 26

<210> 31
<211> 32
<212> DNA
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<223> Description of Artificial Sequence: Primer

<400> 31
atcccgggtc agtcgtgga agtggtgcag ca 32

<210> 32
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 32
gcgagctcgt ccaattttca ctcgggggct tcc 33

<210> 33
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 33
gcgctgcaga ttccatttgg agaggacacg 30

<210> 34
<211> 35
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 34

cgcgggccggc ctcagaagaa ctcgtcaaga aggcg

35

<210> 35

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 35

gctgacacgc caagcctcgc tagtc

25

<210> 36

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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<210> 37

<211> 25

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25

<210> 38

<211> 26

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 38

ggccatggag aacaggaatc tggtagg

26

<210> 39

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 39

gctccgtagt tccaagccag agtag

25

<210> 40

<211> 26

<212> DNA

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<223> Description of Artificial Sequence: Primer

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<210> 41

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 41

gactcgatgc ttcaacgaga ggcag

25

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